



NCBI Training *Offered at Your Institution*

National Center for Biotechnology Information ■ National Library of Medicine ■ National Institutes of Health ■ Department of Health and Human Services

Course Content

GenBank Database: Description and Scope

The NCBI Derivative Databases: RefSeqs

Database Searching Using Entrez

The NCBI Structures Database

- The Molecular Modeling Database
- Viewing Structures and Structural Alignments with Cn3D
- NCBI Gene Expression Resources

Similarity Searching Using NCBI BLAST

- Local Alignment Statistics
- Scoring Systems
- Using WWW BLAST
- PSI-BLAST / PHI-BLAST
- RPS-BLAST (CDD Search)
- Specialized BLAST pages

Genomic Resources at NCBI

- Microbial Genomes
- Higher Genome Resources
 - RefSeq and Entrez Gene
 - UniGene
 - Variation Data (SNPs)
 - The Map Viewer

A Field Guide to GenBank and NCBI Molecular Biology Resources

Molecular sequence databases and computational biology tools are an important part of nearly all areas of biological and biomedical research. To assist life scientists in using these data and tools, the National Center for Biotechnology Information (NCBI) offers, at your institution, a one- to two-day training course entitled, "A Field Guide to GenBank and NCBI Molecular Biology Resources." An overview and list of scheduled locations for the training course is on the Web: www.ncbi.nlm.nih.gov/Class/FieldGuide

This training course is provided free of charge. The NCBI will pay all travel expenses of the instructors within the United States.

Course Description

The course consists of a 3-hour morning lecture followed by a 2-hour instructor-led computer workshop in the afternoon. During the afternoon session, students will gain hands-on experience with the resources at the NCBI site and will learn how to apply these resources in their specific research area. The course provides practical information about GenBank, RefSeq and the integrated genome resources, as well as the other databases maintained at the NCBI. It also provides instruction on effective use of Entrez and BLAST, the two main database search tools.

Intended Audience

The course is designed for principal investigators, postdoctoral fellows, graduate and advanced undergraduate students and others in the life sciences who work with biological sequence data. Both experienced and novice users of the NCBI tools and resources will benefit.

Requirements for Hosting the Course

- A pre-registered audience of at least 50 people
- An auditorium or similar setting with computer projection capabilities
- A multi-workstation computer classroom with internet access and standard web browsers for each machine
- An instructor's workstation with projection capabilities

Note: Multiple hands-on sessions can be offered depending on the number of workstations available and the number of people registered for the course. Additional sessions can be added the following day, if needed.

Instructors

Peter Cooper, Susan Dombrowski, Andrei Gabrielian, Chuong Huynh, Wayne Matten, Rana Morris, Steve Pechous, Vyvy Pham, Eric Sayers, and Tao Tao are bioinformatics training specialists with the NCBI User Services staff.